

SCORE Search Results Details for Application 10010742 and Search Result 20070116_131407_us-10-010-742- 305.oligo.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10010742 and Search Result 20070116_131407_us-10-010-742-305.oligo.rge.

[start](#) | [next page](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2007, 20:52:51 ; Search time 8796 Seconds
(without alignments)
11035.946 Million cell updates/sec

Title: US-10-010-742-305
Perfect score: 1518
Sequence: 1 atggagccctcctggcttca.....ttgcaaaaaaagtttgctaa 1518

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
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4: gb_pl:*
5: gb_pr:*
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10: gb_vi:*
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12: gb_htg:*
13: gb_in:*

14: gb_om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1518	100.0	1518	2	CS110638	CS110638 Sequence
2	1518	100.0	1894	2	AX829108	AX829108 Sequence
3	1518	100.0	2015	2	CS110637	CS110637 Sequence
4	1518	100.0	2015	2	AX317983	AX317983 Sequence
5	1467	96.6	1907	5	AY262056	AY262056 Homo sapi
6	1467	96.6	2020	2	CQ970464	CQ970464 Sequence
7	1467	96.6	2020	2	AX358776	AX358776 Sequence
8	1467	96.6	2020	2	AX362269	AX362269 Sequence
9	1467	96.6	2020	5	AY358631	AY358631 Homo sapi
10	1413	93.1	1548	2	CS110645	CS110645 Sequence
11	1009	66.5	1586	2	AX195182	AX195182 Sequence
12	1009	66.5	1598	2	CS110635	CS110635 Sequence
13	963	63.4	963	2	CS110636	CS110636 Sequence
14	539	35.5	940	2	AX429963	AX429963 Sequence
15	441	29.1	1436	5	AY262057	AY262057 Homo sapi
16	441	29.1	2608	2	CS168612	CS168612 Sequence
17	441	29.1	2608	2	AX834733	AX834733 Sequence
18	441	29.1	2608	5	AK097373	AK097373 Homo sapi
c 19	440	29.0	535	2	CQ431370	CQ431370 Sequence
c 20	419	27.6	535	2	CQ422512	CQ422512 Sequence
21	417	27.5	760	2	CQ429802	CQ429802 Sequence
c 22	397	26.2	444	2	CQ420938	CQ420938 Sequence
c 23	397	26.2	444	2	CQ429812	CQ429812 Sequence
24	384	25.3	397	2	CQ421094	CQ421094 Sequence
c 25	384	25.3	403	2	CQ426106	CQ426106 Sequence
26	384	25.3	598	2	CQ492564	CQ492564 Sequence
27	384	25.3	598	2	CQ496194	CQ496194 Sequence
c 28	379	25.0	379	2	CS110385	CS110385 Sequence
c 29	379	25.0	379	2	AX156195	AX156195 Sequence
30	367	24.2	491	2	CQ422405	CQ422405 Sequence
31	363	23.9	386	2	CQ430462	CQ430462 Sequence
32	362	23.8	498	2	CS110407	CS110407 Sequence
33	362	23.8	498	2	AX156217	AX156217 Sequence
34	351	23.1	526	2	CQ431263	CQ431263 Sequence
35	345	22.7	933	2	BD139838	BD139838 Compounds
36	345	22.7	933	2	AR202942	AR202942 Sequence
37	345	22.7	933	2	AR208043	AR208043 Sequence
38	345	22.7	933	2	AX429916	AX429916 Sequence
c 39	343	22.6	422	2	CQ418336	CQ418336 Sequence
40	333	21.9	393	2	CQ418480	CQ418480 Sequence
41	333	21.9	393	2	CQ421061	CQ421061 Sequence
42	333	21.9	393	2	CQ426250	CQ426250 Sequence
43	327	21.5	658	2	CQ423169	CQ423169 Sequence
44	326	21.5	364	2	CQ426051	CQ426051 Sequence
45	324	21.3	641	2	CQ420928	CQ420928 Sequence

ALIGNMENTS

SCORE Search Results Details for Application 10010742 and Search Result 20070116_131411_us-10-010-742- 305.oligo.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10010742 and Search Result 20070116_131411_us-10-010-742-305.oligo.rni.

[start](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2007, 21:04:49 ; Search time 1641 Seconds
(without alignments)
1730.861 Million cell updates/sec

Title: US-10-010-742-305
Perfect score: 1518
Sequence: 1 atggagccctcctggcttca.....ttgcaaaaaaagtttgctaa 1518

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	539	35.5	940	3	US-09-602-877A-102		Sequence 102, App
2	345	22.7	933	3	US-09-118-554-55		Sequence 55, Appl
3	345	22.7	933	3	US-09-118-627-55		Sequence 55, Appl
4	345	22.7	933	3	US-09-602-877A-55		Sequence 55, Appl
5	35	2.3	266	3	US-09-389-681-414		Sequence 414, App
6	35	2.3	266	3	US-09-620-405B-414		Sequence 414, App
7	35	2.3	266	3	US-09-433-826B-414		Sequence 414, App
8	35	2.3	266	3	US-09-604-287A-414		Sequence 414, App
9	35	2.3	266	3	US-09-834-759-414		Sequence 414, App
10	35	2.3	266	3	US-09-590-751A-414		Sequence 414, App
11	35	2.3	266	3	US-09-551-621-414		Sequence 414, App
12	35	2.3	266	3	US-09-551-621A-414		Sequence 414, App
13	35	2.3	266	3	US-10-076-622-414		Sequence 414, App
14	35	2.3	266	4	US-10-124-805-414		Sequence 414, App
c 15	24	1.6	1508	3	US-09-799-451-109		Sequence 109, App
16	24	1.6	1763	4	US-09-880-107-1610		Sequence 1610, Ap
17	24	1.6	2382	3	US-09-023-655-1436		Sequence 1436, Ap
18	24	1.6	2576	4	US-09-880-107-2138		Sequence 2138, Ap
19	21	1.4	1508	3	US-09-799-451-109		Sequence 109, App
20	21	1.4	1718	3	US-09-799-451-420		Sequence 420, App
21	21	1.4	2071	3	US-10-104-047-720		Sequence 720, App
22	21	1.4	2327	3	US-09-852-067-1		Sequence 1, Appli
23	21	1.4	2327	3	US-10-338-691-1		Sequence 1, Appli
24	21	1.4	31208	3	US-09-852-067-3		Sequence 3, Appli
25	21	1.4	31208	3	US-10-338-691-3		Sequence 3, Appli
26	20	1.3	2084	3	US-09-023-655-1045		Sequence 1045, Ap
27	19	1.3	300	4	US-09-297-648-1885		Sequence 1885, Ap
c 28	19	1.3	880	3	US-09-071-035-495		Sequence 495, App
c 29	19	1.3	880	3	US-10-206-576-495		Sequence 495, App
c 30	19	1.3	1002	3	US-09-107-532A-890		Sequence 890, App
c 31	19	1.3	1005	3	US-09-071-035-493		Sequence 493, App
c 32	19	1.3	1005	3	US-10-206-576-493		Sequence 493, App
33	19	1.3	1557	3	US-09-252-991A-16492		Sequence 16492, A
c 34	19	1.3	1785	3	US-09-252-991A-16007		Sequence 16007, A
c 35	19	1.3	1938	2	US-08-278-635B-1		Sequence 1, Appli
c 36	19	1.3	1938	3	US-08-464-258B-1		Sequence 1, Appli
c 37	19	1.3	1938	3	US-08-471-961-1		Sequence 1, Appli
c 38	19	1.3	1938	3	US-09-345-109C-1		Sequence 1, Appli
c 39	19	1.3	2028	3	US-09-252-991A-16110		Sequence 16110, A
40	19	1.3	2308	3	US-09-270-767-29760		Sequence 29760, A
41	19	1.3	2927	3	US-09-270-767-13738		Sequence 13738, A
c 42	19	1.3	6076	3	US-09-824-734-1		Sequence 1, Appli
c 43	19	1.3	17390	3	US-09-949-016-12910		Sequence 12910, A
c 44	18	1.2	300	4	US-09-297-648-2414		Sequence 2414, Ap
c 45	18	1.2	394	3	US-09-060-756-326		Sequence 326, App

ALIGNMENTS

RESULT 1

US-09-602-877A-102

; Sequence 102, Application US/09602877A

; Patent No. 6432707

**SCORE Search Results Details for Application
10010742 and Search Result
20070116_131416_us-10-010-742-
305.oligo.rnpbn.**

Score Home
Page

Retrieve Application List

SCORE System Overview

SCORE
FAQ

Comments /
Suggestions

This page gives you Search Results detail for the Application 10010742 and Search Result 20070116_131416_us-10-010-742-305.oligo.rnpbn.

[start](#) | [next page](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3950299 seqs, 1456545396 residues

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Word size :      1
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Total number of hits satisfying chosen parameters: 7899788

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	1442	95.0	1906	6	US-10-540-310-3	Sequence 3, Appli
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c 3	614	40.4	1000	8	US-11-266-748A-344927	Sequence 344927,
4	441	29.1	2608	8	US-11-293-697-1857	Sequence 1857, Ap
c 5	320	21.1	753	8	US-11-266-748A-179688	Sequence 179688,
6	320	21.1	753	8	US-11-266-748A-248686	Sequence 248686,
c 7	192	12.6	193471	8	US-11-266-748A-23901	Sequence 23901, A
c 8	158	10.4	1000	8	US-11-266-748A-203310	Sequence 203310,
c 9	158	10.4	1000	8	US-11-266-748A-283212	Sequence 283212,
10	158	10.4	1000	8	US-11-266-748A-309852	Sequence 309852,
c 11	158	10.4	1000	8	US-11-266-748A-392920	Sequence 392920,
12	158	10.4	1000	8	US-11-266-748A-483638	Sequence 483638,
c 13	150	9.9	629	6	US-10-540-310-1	Sequence 1, Appli
c 14	108	7.1	883	8	US-11-266-748A-249501	Sequence 249501,
c 15	87	5.7	600	8	US-11-266-748A-102267	Sequence 102267,
16	87	5.7	600	8	US-11-266-748A-155078	Sequence 155078,
17	70	4.6	746	8	US-11-266-748A-407319	Sequence 407319,
c 18	70	4.6	746	8	US-11-266-748A-478365	Sequence 478365,
19	32	2.1	32	6	US-10-536-560-79632	Sequence 79632, A
20	32	2.1	32	6	US-10-536-560-186809	Sequence 186809,
21	25	1.6	25	7	US-11-371-354-51113	Sequence 51113, A
22	25	1.6	25	7	US-11-371-354-51114	Sequence 51114, A
23	25	1.6	25	7	US-11-371-354-51115	Sequence 51115, A
24	25	1.6	28	6	US-10-536-560-345945	Sequence 345945,
c 25	24	1.6	855	8	US-11-266-748A-1113	Sequence 1113, Ap
26	24	1.6	855	8	US-11-266-748A-62750	Sequence 62750, A
c 27	24	1.6	855	8	US-11-266-748A-65582	Sequence 65582, A
28	24	1.6	1368	7	US-11-371-354-6869	Sequence 6869, Ap
29	24	1.6	1368	7	US-11-371-354-64400	Sequence 64400, A
30	24	1.6	1853	8	US-11-266-748A-254754	Sequence 254754,
31	24	1.6	1853	8	US-11-266-748A-277159	Sequence 277159,
c 32	24	1.6	1853	8	US-11-266-748A-315271	Sequence 315271,
33	24	1.6	2376	8	US-11-293-697-2332	Sequence 2332, Ap
34	21	1.4	21	8	US-11-251-465-298	Sequence 298, App
35	21	1.4	648	7	US-11-371-354-4585	Sequence 4585, Ap
36	21	1.4	648	7	US-11-371-354-58310	Sequence 58310, A
c 37	21	1.4	664	8	US-11-266-748A-17761	Sequence 17761, A
38	21	1.4	1275	10	US-11-299-286-187	Sequence 187, App
39	21	1.4	1413	9	US-11-056-355B-76583	Sequence 76583, A
40	21	1.4	1547	9	US-11-056-355B-106522	Sequence 106522,
41	21	1.4	1547	9	US-11-056-355B-117761	Sequence 117761,
42	21	1.4	1549	9	US-11-056-355B-36314	Sequence 36314, A
43	21	1.4	1555	8	US-11-266-748A-367721	Sequence 367721,
c 44	21	1.4	1555	8	US-11-266-748A-451100	Sequence 451100,
45	21	1.4	2343	6	US-10-131-833A-107	Sequence 107, App

ALIGNMENTS

RESULT 1

US-10-540-310-3

; Sequence 3, Application US/10540310

SCORE Search Results Details for Application 10010742 and Search Result \$itemName.

Comments /
Suggestions

This page gives you Search Results detail for the Application 10010742 and Search Result \$itemName.

[start](#) | [next page](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

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Run on:      January 18, 2007, 20:34:00 ; Search time 941 Seconds
              (without alignments)
              11247.474 Million cell updates/sec
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Title:          US-10-010-742-305
Perfect score:  1518
Sequence:       1 atggagccctcctggcttca.....ttgcaaaaaaagtttgctaa 1518
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1518	100.0	1518	7	ADU01524	Adu01524 Breast ca
2	1518	100.0	1518	7	ADZ41788	Adz41788 Human bre
3	1518	100.0	1894	6	ABT07693	Abt07693 Breast ca
4	1518	100.0	2015	6	AAD24015	Aad24015 Human dru
5	1518	100.0	2015	7	ADU01523	Adu01523 Breast ca
6	1518	100.0	2015	7	ADZ41787	Adz41787 Human bre
7	1467	96.6	1518	12	ADQ48399	Adq48399 Human cyt
8	1467	96.6	1975	10	AAD60551	Aad60551 Human cyt
9	1467	96.6	1975	10	ACA61906	Aca61906 cDNA enco
10	1467	96.6	1975	12	ADQ48397	Adq48397 Human cyt
11	1467	96.6	2020	6	ABK33550	Abk33550 cDNA enco
12	1467	96.6	2020	7	ADY31769	Ady31769 Novel hum
13	1467	96.6	2020	8	ACA68511	Aca68511 Novel hum
14	1467	96.6	2020	9	ABT44240	Abt44240 Human PRO
15	1467	96.6	2020	9	ABT44523	Abt44523 Human PRO
16	1467	96.6	2020	9	ACD82190	Acd82190 Human sec
17	1467	96.6	2020	9	ABT43896	Abt43896 Human mem
18	1467	96.6	2020	9	ADB83519	Adb83519 Novel hum
19	1467	96.6	2020	9	ADB80625	Adb80625 Novel hum
20	1467	96.6	2020	9	ADB73166	Adb73166 Novel hum
21	1467	96.6	2020	9	ADB78248	Adb78248 Novel hum
22	1467	96.6	2020	10	ADB84896	Adb84896 Human PRO
23	1467	96.6	2020	10	ADB78002	Adb78002 Novel hum
24	1467	96.6	2020	10	ADB87068	Adb87068 Human PRO
25	1467	96.6	2020	10	ADB84650	Adb84650 Human PRO
26	1467	96.6	2020	10	ADB83765	Adb83765 Novel hum
27	1467	96.6	2020	10	ADB72920	Adb72920 Novel hum
28	1467	96.6	2020	10	ADC36758	Adc36758 Human PRO
29	1467	96.6	2020	10	ADC21748	Adc21748 Human PRO
30	1467	96.6	2020	10	ADC49779	Adc49779 Novel hum
31	1467	96.6	2020	10	ADC48978	Adc48978 Novel hum
32	1467	96.6	2020	10	ADC49495	Adc49495 Novel hum
33	1467	96.6	2020	10	ADC47356	Adc47356 Novel hum
34	1467	96.6	2020	10	ADC47101	Adc47101 Novel hum
35	1467	96.6	2020	10	ADC77976	Adc77976 Novel hum
36	1467	96.6	2020	10	ADD06211	Add06211 Novel hum
37	1467	96.6	2020	10	ADC77730	Adc77730 Novel hum
38	1467	96.6	2020	10	ADD50693	Add50693 Novel hum
39	1467	96.6	2020	10	ADD50939	Add50939 Novel hum
40	1467	96.6	2020	10	ADD50420	Add50420 Human PRO
41	1467	96.6	2020	10	ADD50174	Add50174 Human PRO
42	1467	96.6	2020	10	ADD51185	Add51185 Novel hum
43	1467	96.6	2020	10	ACA66855	Aca66855 cDNA enco
44	1467	96.6	2020	10	ACD68607	Acd68607 Novel hum
45	1467	96.6	2020	12	ADC48732	Adc48732 Novel hum

ALIGNMENTS

RESULT 1

ADU01524

ID ADU01524 standard; cDNA; 1518 BP.

SCORE Search Results Details for Application 10010742 and Search Result 20070116_131409_us-10-010-742- 305.oligo.rst.

[Score Home](#)
[Page](#)

[Retrieve Application](#)
[List](#)

[SCORE System](#)
[Overview](#)

[SCORE](#)
[FAQ](#)

[Comments /](#)
[Suggestions](#)

This page gives you Search Results detail for the Application 10010742 and Search Result 20070116_131409_us-10-010-742-305.oligo.rst.

[start](#) | [next page](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2007, 21:00:56 ; Search time 11159 Seconds
(without alignments)
7606.913 Million cell updates/sec

Title: US-10-010-742-305
Perfect score: 1518
Sequence: 1 atggagccctcctggcttca.....ttgcaaaaaagtttgctaa 1518

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	575	37.9	703	9	DN998330	DN998330 TC123874
	2	571	37.6	792	2	BG193485	BG193485 RST12619
	3	508	33.5	557	9	DA999608	DA999608 DA999608
	4	508	33.5	558	9	DB002610	DB002610 DB002610
	5	508	33.5	568	9	DA999542	DA999542 DA999542
	6	497	32.7	538	9	DB005939	DB005939 DB005939
	7	450	29.6	788	2	BG201072	BG201072 RST20398
	8	440	29.0	737	2	BG210988	BG210988 RST30544
	9	399	26.3	787	2	BG218514	BG218514 RST38137
	10	388	25.6	575	9	DA999639	DA999639 DA999639
	11	374	24.6	777	2	BG219391	BG219391 RST39149
	12	320	21.1	535	1	AI733538	AI733538 yl48g04.y
	13	320	21.1	548	1	AI820775	AI820775 yl38c11.y
	14	320	21.1	663	4	BX094680	BX094680 BX094680
	15	284	18.7	432	10	H25624	H25624 yl48g04.r1
	16	274	18.1	807	2	BG212152	BG212152 RST31623
	17	272	17.9	767	2	BG192933	BG192933 RST12058
c	18	210	13.8	629	1	AI668594	AI668594 yl38c11.x
c	19	201	13.2	760	1	AV700083	AV700083 AV700083
	20	188	12.4	252	2	BG204180	BG204180 RST23576
	21	181	11.9	462	14	DQ044760	DQ044760 Homo sapi
	22	177	11.7	584	9	DB222508	DB222508 DB222508
	23	175	11.5	569	9	DA998990	DA998990 DA998990
c	24	168	11.1	861	2	BG217894	BG217894 RST37618
c	25	150	9.9	629	1	AI668602	AI668602 yl48g04.x
	26	146	9.6	267	2	BG214692	BG214692 RST34341
c	27	146	9.6	882	2	BG196467	BG196467 RST15689
c	28	142	9.4	859	2	BG205754	BG205754 RST25188
	29	136	9.0	332	10	H21976	H21976 yl38c11.r1
	30	134	8.8	451	14	DQ037005	DQ037005 Homo sapi
	31	130	8.6	294	10	DW422693	DW422693 HHAGE0224
	32	119	7.8	218	11	AY758967	AY758967 CH255-13m
	33	115	7.6	536	9	DB000263	DB000263 DB000263
c	34	110	7.2	623	1	AA193450	AA193450 zr40e07.r
	35	108	7.1	469	1	AI675602	AI675602 wc02e11.x
	36	108	7.1	618	8	CN480497	CN480497 UI-H-DI0-
	37	108	7.1	715	11	AQ394813	AQ394813 CITBI-E1-
	38	91	6.0	446	14	DQ037006	DQ037006 Pan trogl
	39	87	5.7	602	4	CA440572	CA440572 UI-H-DI0-
	40	86	5.7	729	11	AQ505963	AQ505963 RPCI-11-3
c	41	85	5.6	822	2	BG213096	BG213096 RST32700
c	42	81	5.3	858	2	BG196956	BG196956 RST16188
	43	70	4.6	317	14	DQ044761	DQ044761 Pan trogl
c	44	66	4.3	877	2	BG192934	BG192934 RST12059
	45	58	3.8	498	11	AQ450557	AQ450557 HS_5166_A

ALIGNMENTS

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

```
Run on:      January 18, 2007, 21:17:41 ; Search time 2058 Seconds
              (without alignments)
              9063.474 Million cell updates/sec
```

Title: US-10-010-742-305
Perfect score: 1518
Sequence: 1 atggagccctcctggcttca.....ttgcaaaaaaagtgttqctaa 1518

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37781012

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

```
Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
```

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1518	100.0	1518	3	US-09-910-689-305	Sequence 305, App
2	1518	100.0	1518	6	US-10-010-742-305	Sequence 305, App
3	1518	100.0	1518	8	US-10-717-296-305	Sequence 305, App
4	1518	100.0	1894	8	US-10-058-270A-1	Sequence 1, Appli
5	1518	100.0	2015	3	US-09-910-689-304	Sequence 304, App
6	1518	100.0	2015	6	US-10-010-742-304	Sequence 304, App
7	1518	100.0	2015	8	US-10-296-606-23	Sequence 23, Appl
8	1518	100.0	2015	8	US-10-717-296-304_	Sequence 304, App
9	1467	96.6	1518	6	US-10-067-668-3	Sequence 3, Appli
10	1467	96.6	1518	6	US-10-175-696-3	Sequence 3, Appli
11	1467	96.6	1518	8	US-10-776-871-3	Sequence 3, Appli
12	1467	96.6	1975	6	US-10-067-668-1	Sequence 1, Appli
13	1467	96.6	1975	6	US-10-175-696-1	Sequence 1, Appli
14	1467	96.6	1975	8	US-10-776-871-1	Sequence 1, Appli
15	1467	96.6	2020	6	US-10-227-884-29	Sequence 29, Appl
16	1467	96.6	2020	6	US-10-230-163-29	Sequence 29, Appl
17	1467	96.6	2020	6	US-10-230-338-29	Sequence 29, Appl
18	1467	96.6	2020	6	US-10-218-631-29	Sequence 29, Appl
19	1467	96.6	2020	6	US-10-230-414-29	Sequence 29, Appl
20	1467	96.6	2020	6	US-10-232-224-29	Sequence 29, Appl
21	1467	96.6	2020	6	US-10-216-159A-29	Sequence 29, Appl
22	1467	96.6	2020	6	US-10-218-849-29	Sequence 29, Appl
23	1467	96.6	2020	6	US-10-227-873-29	Sequence 29, Appl
24	1467	96.6	2020	6	US-10-227-883-29	Sequence 29, Appl
25	1467	96.6	2020	6	US-10-219-076-29	Sequence 29, Appl
26	1467	96.6	2020	6	US-10-230-434-29	Sequence 29, Appl
27	1467	96.6	2020	6	US-10-219-003-29	Sequence 29, Appl
28	1467	96.6	2020	6	US-10-219-075-29	Sequence 29, Appl
29	1467	96.6	2020	6	US-10-219-464-29	Sequence 29, Appl
30	1467	96.6	2020	6	US-10-219-466-29	Sequence 29, Appl
31	1467	96.6	2020	6	US-10-219-479-29	Sequence 29, Appl
32	1467	96.6	2020	6	US-10-219-481-29	Sequence 29, Appl
33	1467	96.6	2020	6	US-10-230-260-29	Sequence 29, Appl
34	1467	96.6	2020	6	US-10-232-231-29	Sequence 29, Appl
35	1467	96.6	2020	6	US-10-232-233-29	Sequence 29, Appl
36	1467	96.6	2020	6	US-10-216-165-29	Sequence 29, Appl
37	1467	96.6	2020	6	US-10-218-956-29	Sequence 29, Appl
38	1467	96.6	2020	6	US-10-219-468-29	Sequence 29, Appl
39	1467	96.6	2020	6	US-10-219-478-29	Sequence 29, Appl
40	1467	96.6	2020	6	US-10-219-536-29	Sequence 29, Appl
41	1467	96.6	2020	6	US-10-233-205-29	Sequence 29, Appl
42	1467	96.6	2020	6	US-10-219-072-29	Sequence 29, Appl
43	1467	96.6	2020	6	US-10-219-470-29	Sequence 29, Appl
44	1467	96.6	2020	6	US-10-219-474-29	Sequence 29, Appl
45	1467	96.6	2020	6	US-10-219-524-29	Sequence 29, Appl

ALIGNMENTS